WHAT IS CLAIMED IS:

1. An isolated DNA molecule comprising a promoter or biologically active fragment thereof or variant of these, wherein the promoter is located upstream of a transcribable DNA sequence that hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low stringency conditions.

2. The DNA molecule of claim 1, wherein the transcribable DNA sequence is obtained from a virus.

3. The DNA molecule of claim 1, wherein the transcribable DNA sequence is obtained from a badnavirus.

4. The DNA molecule of claim 2 or claim 3, wherein the transcribable DNA sequence is expressed constitutively in a monocotyledonous plant.

5. The DNA molecule of claim 2 or claim 3, wherein the transcribable DNA sequence is expressed constitutively in a non-graminaceous monocotyledonous plant.

6. The DNA molecule of claim 5, wherein the non-graminaceous monocotyledonous plant is selected from the group consisting of *Musaceae*, taro, ginger, onions, garlic, pineapple, bromeliaeds, palms, orchids, lilies and irises.

7. The DNA molecule of claim 5, wherein the non-graminaceous monocotyledonous plant is taro.

8. The DNA molecule of claim 1, wherein the promoter comprises the sequence set forth in SEQ ID NO:6.

9. The DNA molecule of claim 8, wherein the biologically active fragment is selected from the group consisting of SEQ ID NO:7, 8 and 9.

10. The DNA molecule of claim 8, wherein the variant has at least 30% sequence identity to a sequence selected from the group consisting of SEQ ID NO:6, 7, 8 and 9.

11. The DNA molecule of claim 8, wherein the variant is capable of hybridising to a sequence selected from the group consisting of SEQ ID NO: 6, 7, 8 and 9 under at least low stringency conditions.

12. An isolated polynucleotide comprising a nucleotide sequence that corresponds or is complementary to at least a portion of the sequence set forth in SEQ ID NO:1 or to a variant thereof.

13. The polynucleotide of claim 12, wherein the variant displays at least 30% sequence identity to at least a portion of the sequence set forth in SEQ ID NO:1, which is at least 18 nucleotides in length.

14. The polynucleotide of claim 13, wherein the variant displays at least 30% sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO:3, 4 and 5.

15. The polynucleotide of claim 12, wherein the variant hybridises to at least a portion of the sequence set forth in SEQ ID NO:1, which is at least 18 nucleotides in length, under at least low stringency conditions.

16. The polynucleotide of claim 15, wherein the variant hybridises to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO:3, 4 and 5 under at least low stringency conditions.

17. An isolated polypeptide comprising an amino acid sequence that corresponds to at least a portion of the sequence set forth in any of SEQ ID NO:3, 4 or 5 or of a variant that displays at least 30% sequence identity to that sequence, wherein the portion is at least 6 amino acid residues in length.

18. A chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low stringency conditions, wherein the promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed.

19. The construct of claim 18, further comprising a 3' non-translated sequence that is operably linked to the foreign or endogenous DNA sequence and that functions in plant cells to terminate transcription and/or to cause addition of a polyadenylated nucleotide sequence to the 3' end of a transcribed RNA sequence.

20. The construct of claim 18, wherein the promoter comprises the sequence set forth in SEQ ID NO:6.

21. The construct of claim 18, wherein the biologically active fragment is selected from the group consisting of SEQ ID NO:7, 8 and 9.

22. The construct of claim 18, wherein the variant has at least 30% sequence identity to a sequence selected from the group consisting of SEQ ID NO:6,7, 8 and 9.

23. The construct of claim 18, wherein the variant is capable of hybridising to a sequence selected from the group consisting of SEQ ID NO: 6,7, 8 and 9 under at least low stringency conditions.

24. The construct of claim 18, wherein the foreign or endogenous DNA sequence encodes a structural or regulatory protein.

25. The construct of claim 18, wherein the foreign or endogenous DNA sequence encodes a transcript capable of modulating expression of a corresponding target gene.

26. The construct of claim 25, wherein the transcript comprises a transcribed region aimed at downregulating the expression of the corresponding target gene.

27. The construct of claim 25, wherein the transcript comprises a transcribed region that represents a molecule selected from the group consisting of a sense suppression molecule, an antisense RNA, a ribozyme and an RNAi molecule.

28. The construct of claim 18, further comprising an enhancer element.

29. The construct of claim 18, further comprising a leader sequence which modulates mRNA stability.

30. The construct of claim 18, further comprising a targeting sequence for targeting a protein product of the foreign or endogenous DNA sequence to an intracellular compartment within plant cells or to an extracellular environment.

31. The construct of claim 18, further comprising a selectable marker gene.

32. The construct of claim 18, further comprising a screenable marker gene.

33. The construct of claim 18, wherein the promoter or biologically active fragment or variant is constitutively expressed in a host cell.

34. The construct of claim 33, wherein the host cell is a plant cell.

35. The construct of claim 33, wherein the host cell is a monocotyledonous plant cell.

36. The construct of claim 33, wherein the host cell is a non-graminaceous monocotyledonous plant cell.

37. The construct of claim 33, wherein the host cell is a non-graminaceous monocotyledonous plant cell selected from the group consisting of *Musaceae*, taro, ginger, onions, garlic, pineapple, bromeliaeds, palms, orchids, lilies and irises.

38. The construct of claim 33, wherein the host cell is a graminaceous monocotyledonous plant cell.

39. The construct of claim 33, wherein the host cell is a dicotyledonous plant cell.

40. A method for gene expression in a plant, comprising introducing into a plant cell a chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low stringency conditions, wherein the promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed

41. A method for producing transformed plant cells, comprising:

(a) introducing into regenerable plant cells a chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low stringency conditions, wherein the promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed, so as to yield transformed plant cells; and

(b) identifying or selecting transformed plant cells.

42. A method for selecting stable genetic transformants from transformed plant cells comprising:

(a) introducing into regenerable plant cells a chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low stringency conditions, wherein the promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed, so as to yield transformed plant cells; and

(b) identifying or selecting a transformed plant cell line from said transformed plant cells.

43. A method for producing a differentiated transgenic plant, comprising:

(a) introducing into regenerable plant cells a chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low stringency conditions, wherein the promoter or biologically active fragment or variant

is operably linked to a foreign or endogenous DNA sequence to be transcribed, so as to yield regenerable transformed plant cells;

(b) identifying or selecting a population of transformed plant cells; and

(c) regenerating a differentiated transgenic plant from the population.

44. The method of any one of claims 40 to 43, wherein the cells are dicotyledonous plant cells.

45. The method of any one of claims 40 to 43, wherein the cells are monocotyledonous plant cells.

46. The method of any one of claims 40 to 43, wherein the cells are graminaceous monocotyledonous plant cells.

47. The method of any one of claims 40 to 43, wherein the cells are non-graminaceous monocotyledonous plant cells.

48. The method of any one of claims 40 to 43, wherein expression of the chimeric DNA construct in the transformed cells imparts a phenotypic characteristic to the transformed cells.

49. The method of any one of claim 40 to 43, wherein the construct comprises a selectable marker gene.

50. The method of any one of claim 40 to 43, wherein the construct comprises a screenable marker gene.

51. The method of claim 43, wherein expression of the chimeric DNA construct renders the differentiated transgenic plant identifiable over the corresponding non-transgenic plant.

52. The method of claim 43, further comprising obtaining progeny from the differentiated transgenic plant.

53. Progeny obtained by the method of claim 52.

54. A plant part of the differentiated transgenic plant obtained from the method of claim 43, wherein the plant part contains the chimeric construct.

55. A differentiated transgenic plant regenerated from transformed plant cells obtained by the method of claim 41.

56. A transformed plant cell containing a chimeric DNA construct comprising an isolated plant promoter or biologically active fragment thereof or variant of these, wherein said promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low

stringency conditions, wherein said promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed.

57. A differentiated transgenic plant comprising plant cells containing a chimeric DNA construct comprising an isolated plant promoter or biologically active fragment thereof or variant of these, wherein said promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low stringency conditions, wherein said promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed.

58. The transgenic plant of claim 57, wherein the plant is a dicotyledonous plant.

59. The transgenic plant of claim 57, wherein the plant is a monocotyledonous plant.

60. The transgenic plant of claim 57, wherein the plant is a graminaceous monocotyledonous plant.

61. The transgenic plant of claim 57, wherein the plant is a non-graminaceous monocotyledonous plant.

62. The transgenic plant of claim 57, wherein the construct comprises a selectable marker gene.

63. The transgenic plant of claim 57, wherein the construct comprises a screenable marker gene.

64. The transgenic plant of claim 57, wherein the expression of the chimeric DNA construct renders the differentiated transgenic plant identifiable over the corresponding non-transgenic plant.

65. Use of a chimeric DNA construct comprising an isolated plant promoter or biologically active fragment thereof or variant of these, wherein said promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least low stringency conditions, wherein said promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed, in the production of a transformed plant cell, plant or plant part.

66. A method for diagnosing a badnaviral infection of a plant, comprising detecting the presence in a cell or tissue of the plant of (a) a nucleotide sequence that corresponds or is complementary to at least a portion of the nucleotide sequence set forth in SEQ ID NO:1 or 2, or of a variant of the nucleotide sequence, or (b) an amino acid sequence that corresponds to at least a portion of the sequence set forth in SEQ ID NO:3, 4 or 5, or of a variant of the amino acid sequence.

67. A method of screening for an agent that modulates badnaviral infection, the method comprising:

– contacting a preparation comprising:

(i) a polypeptide comprising an amino acid sequence that corresponds to at least a portion of the sequence set forth in SEQ ID NO: 3, 4 or 5, or of a variant of the sequence; or

(ii) a polynucleotide comprising a nucleotide sequence that corresponds or is complementary to at least a portion of the sequence set forth in SEQ ID NO:1 or 2, which polynucleotide is operably linked to a promoter; or

(iii) a polynucleotide comprising a reporter gene that is operably connected to a promoter comprising the sequence set forth in SEQ ID NO:6, 7, 8 or 9,

with a test agent; and

– detecting a change in the level and/or functional activity of the polypeptide, or an expression product of the nucleotide sequence or of the reporter gene, relative to a normal or reference level and/or functional activity in the absence of the test agent.

68. The method of claim 67, wherein the agent inhibits or reduces badnavirus infection and the method comprises detecting a reduction in the level and/or functional activity of the polypeptide, or an expression product of the nucleotide sequence or of the reporter gene, relative to the normal or reference level and/or functional activity.

69. A method for treating and/or preventing badnaviral infection of a plant, comprising administering to the plant an agent that:

– reduces the level and/or functional activity of:

a polypeptide that comprises an amino acid sequence corresponding to at least a portion of the sequence set forth in SEQ ID NO: 3, 4 or 5, or of a variant of the sequence; or

an expression product of a nucleotide sequence that corresponds or is complementary to at least a portion of the sequence set forth in SEQ ID NO:1 or 2; or

– reduces the functional activity of a promoter that comprises the sequence set forth in any one of SEQ ID NO:6, 7, 8 or 9.